GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 30, 2003, 00:35:07 ; Search time 235.597 Seconds
(without alignments)
12904.233 Million cell updates/sec

Title: US-09-768-781-1
Perfect score: 1350
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	525.2	38.9	532	24	ABL89709	Human polynucleoti
	2	513.8	38.1	531	23	ABK41708	cDNA encoding nove
	3	289.6	21.5	5096	24	ABL64686	Stomach cancer rel
	4	282.8	20.9	5215	24	ABN59695	Novel human coding
	5	270.6	20.0	668	22	ABA46582	Human breast cell
	6	270.6	20.0	668	22	ABA64445	Human foetal liver
	7	270.6	20.0	668	22	ABA31582	Probe #10048 for g
	8	270.6	20.0	668	22	AAK12903	Human brain expres
	9	270.6	20.0	668	22	AAK38630	Human bone marrow
	10	270.6	20.0	668	22	AAI19430	Probe #9363 for ge
	11	270.6	20.0	668	22	AAI44621	Probe #13307 used
	12	270.6	20.0	668	22	AAI05155	Probe #5146 used t
	13	270.6	20.0	668	24	ABS12699	Human genome-deriv
	14	176.8	13.1	471	22	ABA51767	Human foetal liver
	15	176.8	13.1	471	22	ABA21596	Probe #62 for gene
	16	176.8	13.1	471	22	AAK00075	Human brain expres
	17	176.8	13.1	471	22	AAK25512	Human bone marrow
	18	176.8	13.1	471	22	AAI10135	Probe #68 for gene
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	20	176.8	13.1	471	22	AAI00076	Probe #67 used to
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c	23	160.4	11.9	384	22	ABA36103	Probe #14569 for g
c	24	160.4	11.9	384	22	AAK17479	Human brain expres
	25	160.2	11.9	626	22	AAF93700	cDNA encoding SRT
c	26	140.4	10.4	498	22	ABA26217	Probe #4683 for ge
c	27	140.4	10.4	498	22	AAK04747	Human brain expres
	28	73.2	5.4	294	22	ABA48894	Human breast cell
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	32	73.2	5.4	294	22	AAK40967	Human bone marrow
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	41	65	4.8	477	22	AAK27964	Human bone marrow
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	44	65	4.8	477	22	AAI02452	Probe #2443 used t
	45	65	4.8	477	24	ABS02431	Human genome-deriv

ALIGNMENTS

RESULT 1
ABL89709
ID ABL89709 standard; cDNA; 532 BP.
XX
AC ABL89709;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 271.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR P-PSDB; ABB89300.

```
XX
PT   Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT   prevention of neural, immune system, muscular, reproductive,
PT   gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT   disorders -
XX
PS   Claim 4; SEQ ID NO 271; 2081pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC   (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC   in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC   and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC   epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC   and parasitic infections.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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SQ   Sequence 532 BP; 109 A; 129 C; 121 G; 168 T; 5 other;

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AC   ABK41708;
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DT   21-MAY-2002  (first entry)
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DE   cDNA encoding novel human connective tissue related polypeptide #96.
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KW   Human; connective tissue related disorder; cancer; gene therapy;
KW   cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155343-A1.
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PF   17-JAN-2001; 2001WO-US01322.
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PR   04-FEB-2000; 2000US-0180628.
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PR 14-SEP-2000; 2000US-0232400.
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PR 08-NOV-2000; 2000US-0246611.
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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-565190/63.
DR P-PSDB; AAU86530.
XX
PT Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder
PT such as cancer or rheumatoid arthritis -
XX
PS Claim 4; SEQ ID No 106; 673pp; English.
XX
CC The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful
CC in gene therapy. ABK41613-ABK42101 represent cDNA sequences encoding
CC the novel human connective tissue related polypeptides.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 531 BP; 109 A; 128 C; 121 G; 168 T; 5 other;

Query Match 38.1%; Score 513.8; DB 23; Length 531;
Best Local Similarity 98.5%; Pred. No. 1.8e-147;
Matches 523; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

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Qy    807 TGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGATTAAGTTCTG 866
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Db     62 TGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGATTAAGTTCTG 121

Qy    867 GAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGTCGGCACTCT 926
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RESULT 3
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XX
AC ABL64686;
XX
DT 15-MAY-2002 (first entry)
XX
DE Stomach cancer related gene sequence SEQ ID NO:3023.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
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PR 05-JUN-2000; 2000US-209473P.
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PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1; SEQ ID 3023; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 5096 BP; 1392 A; 1064 C; 1022 G; 1618 T; 0 other;

Query Match 21.5%; Score 289.6; DB 24; Length 5096;
Best Local Similarity 54.6%; Pred. No. 7.3e-78;
Matches 627; Conservative 0; Mismatches 509; Indels 12; Gaps 2;

```
Qy    118 TCCACCTTTTTGTACTGTGGGGAGGCTGCATCTGCTTTGTACATGGTTAGAATCTATCGA 177
          |||   ||  ||| |   |  ||| |  |  | ||  |   | ||   || | ||| ||
Db    110 TCCGTGTTCCTGTTCGTGGCCGAGACAACGGCGGCGCTCAGCCTGAGCAGCACCTACCGC 169

Qy    178 AAGAATAGTGAAACTTACCGGATGACATACACCTTTTCTTTCTTTATGTTTTCATCCATT 237
          |    | ||          ||  | |    || ||  |||||   |  |  | | |
Db    170 TCGGGCGGGGACCGCATGTGGCAGGCGCTGACGTTGCTTTTCTCGCTACTGCCTTGCGCG 229

Qy    238 ATGGTCCAGTTGACCCTCATTTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCA 297
          | || ||| | || ||  | || || ||| | || ||   |   ||    |||||    |
Db    230 CTCGTGCAGCTCACGCTTCTCTTCGTACACCGCGACCTCAGCCGCGACCGCCCGCTCGTA 289

Qy    298 TTATTTATGCATCTAATCCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAG 357
          |  |  |||| ||  | |    | || ||  || |||| ||||| || | | |    |
Db    290 CTGCTGCTGCACCTGCTGCAACTTGGGCCCCTTTTCAGGTGTTTTGAAGTCTTCTGCATC 349

Qy    358 TACCTCACACTGTGGAAGAAAGAGGAGCAGGAGGAGCCCTATGTCAGCCTCACCCGAAAG 417
          |||  |            ||  ||   |  | || |||||  ||||||||  |||||   |||
Db    350 TACTTTC---------AGTCAGGCAACAATGAAGAGCCTTATGTCAGTATCACCAAGAAG 400

Qy    418 AAG---ATGCTAATAGATGGCGAGGAGGTGCTGATAGAATGGGAGGTGGGCCACTCCATC 474
          | |   |||| || | |||||       | |  ||| ||   ||||||||||||  |
Db    401 AGGCAAATGCCAAAAAATGGCCTCTCAGAGGAGATTGAGAAGGAGGTGGGCCAGGCAGAA 460

Qy    475 CGGACCCTGGCTATGCACCGCAATGCCTACAAACGTATGTCACAGATCCAAGCCTTCCTG 534
          | |  ||    |  |||||     || | ||  ||   |||   |||||| || ||| ||
Db    461 GGCAAACTAATCACCCACCGATCAGCGTTCAGCCGGGCGTCGGTGATCCAGGCTTTCTTG 520

Qy    535 GGCTCAGTGCCCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGCAGAGGTTCCC 594
          |||||||  ||||||||||||   ||||| ||  | ||  | ||          || ||  |
Db    521 GGCTCAGCCCCCCAGCTGACCCTACAGCTGTACATAAGTGTCATGCAGCAGGACGTCACT 580

Qy    595 CTGGGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTT 654
          | || |||  | | || |||    | |||||| | ||  |     ||||| ||||   |
Db    581 GTTGGAAGAAGTCTCCTCATGACCATATCCCTGTTGTCCATTGTGTATGGAGCCTTGCGC 640

Qy    655 TGCAATATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTTGGGCCACTA 714
          |||||  ||  | || ||| | ||||||||||||||| ||  |  |      |  ||| ||
Db    641 TGCAACATCCTAGCCATCAAAATCAAGTACGATGAGTATGAAGTCAAAGTGAAGCCTCTG 700
```

```
Qy    715 GAAGTCCTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTG 774
          |  |||| |||  | | ||| |||  || |||||  |  | ||  |  |  | |||
Db    701 GCCTATGTCTGTATCTTCCTGTGGAGGAGCTTTGAGATTGCCACTCGAGTTGTAGTCCTG 760

Qy    775 GTGCTCTTCTCAGCCACTTTGAAATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTG 834
          || |||||  |  ||    ||||       ||  |||    |  || |  |||||||| |
Db    761 GTCCTCTTTACCTCCGTCCTGAAGACCTGGGTGGTGGTTATAATACTCATCAACTTCTTC 820

Qy    835 ATCATCCTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAAC 894
          |   || ||||  | ||||||||     |||||| | |||||| |||   | ||  | |||
Db    821 AGTTTCTTCTTGTACCCCTGGATCCTCTTCTGGTGCAGTGGTTCCCCATTCCCTGAGAAC 880

Qy    895 ATTGAGAAAAACTTCAGCCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTC 954
          || |||||   | ||||  |.|| |||||     | || ||    |.  | ||  | |||
Db    881 ATAGAGAAGGCCCTCAGTAGAGTGGGCACCACCATTGTACTATGCTTTCTAACTTTACTC 940

Qy    955 TATGCTGGCATCAACTTCTCTTGCTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGAT 1014
          ||| |||| |||||| | |  |||||||| ||| | ||| |||   | |     |   ||
Db    941 TATACTGGTATCAACATGTTCTGCTGGTCTGCTGTACAGCTGAAAATTGACAGCCCTGAC 1000

Qy    1015 CTCGTCGACAAAGGGCAGAACTGGGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTA 1074
           ||| ||  |||    || || |||   ||  |    || | || |  | ||| ||  |
Db    1001 CTCATCAGCAAGTCCCATAATTGGTACCAGCTACTGGTGTATTACATGATAAGATTCATC 1060

Qy    1075 GAGAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTAC 1134
           |||||||  ||| |  || |  | |   |  | ||         | | |   || ||
Db    1061 GAGAATGCCATCCTCCTCCTCCTGTGGTATCTTTTCAAGACTGACATCTATATGTATGTG 1120

Qy    1135 TGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGACTTCATG 1194
           ||     |  || | | |||||||  | |||| ||     |  |||||  |||||||
Db    1121 TGCGCACCTCTGTTGGTCCTGCAGCTGCTCATTGGGTACTGCACAGCCATTCTCTTCATG 1180

Qy    1195 CTCCTTTTCTTCCAGTACTTGCATCCATTGCGCTCACTCTTCACCCATAATGTAGTAGAC 1254
           ||  | ||||  |||| ||| || || |       |||||  |    | |||    ||
Db    1181 CTTGTATTCTATCAGTTCTTCCACCCTTGCAAAAAGCTCTTTTCTTCCAGTGTTTCTGAA 1240

Qy    1255 TACCTCCA 1262
             | | ||
Db    1241 GGCTTTCA 1248
```

RESULT 4
ABN59695
ID ABN59695 standard; cDNA; 5215 BP.
XX
AC ABN59695;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 106.
XX
KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US26015.
XX
PR 11-SEP-2000; 2000US-0659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR P-PSDB; ABB97282.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
PS Claim 1; SEQ ID NO 106; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention.
XX
SQ Sequence 5215 BP; 1458 A; 1058 C; 1035 G; 1664 T; 0 other;

Query Match 20.9%; Score 282.8; DB 24; Length 5215;
Best Local Similarity 55.7%; Pred. No. 9.1e-76;
Matches 589; Conservative 0; Mismatches 457; Indels 12; Gaps 2;

```
Qy    208 ACCTTTTCTTTCTTTATGTTTTCATCCATTATGGTCCAGTTGACCCTCATTTTTGTCCAC 267
          || ||   |||||   |  |  | | |    | || ||| | || ||  | || || |||
Db    319 ACGTTGCTTTTCTCGCTACTGCCTTGCGCGCTCGTGCAGCTCACGCTTCTCTTCGTACAC 378

Qy    268 AGAGATCTAGCCAAAGATAAACCGCTATCATTATTTATGCATCTAATCCTCTTGGGACCT 327
          | || ||   |   ||    |||||   | |  |  |||| ||  | |   | || ||
Db    379 CGCGACCTCAGCCGCGACCGCCCGCTCGTACTGCTGCTGCACCTGCTGCAACTTGGGCCC 438

Qy    328 GTTATCAGATGTTTGGAGGCCATGATTAAGTACCTCACACTGTGGAAGAAAGAGGAGCAG 387
          || |||| ||||| || | | |    |  ||| |           ||  ||   |  |
Db    439 CTTTTCAGGTGTTTTGAAGTCTTCTGCATCTACTTTC---------AGTCAGGCAACAAT 489

Qy    388 GAGGAGCCCTATGTCAGCCTCACCCGAAAGAAG---ATGCTAATAGATGGCGAGGAGGTG 444
          || ||||| ||||||||  |||||   |||| |   |||| || | |||||       | |
Db    490 GAAGAGCCTTATGTCAGTATCACCAAGAAGAGGCAAATGCCAAAAAATGGCCTCTCAGAG 549

Qy    445 CTGATAGAATGGGAGGTGGGCCACTCCATCCGGACCCTGGCTATGCACCGCAATGCCTAC 504
            ||| ||   ||||||||||||  |    | |  ||    |  |||||    || | |
Db    550 GAGATTGAGAAGGAGGTGGGCCAGGCAGAAGGCAAACTAATCACCCACCGATCAGCGTTC 609

Qy    505 AAACGTATGTCACAGATCCAAGCCTTCCTGGGCTCAGTGCCCCAGCTGACCTATCAGCTC 564
          |  ||   |||   |||||| || ||| |||||||||  ||||||||||  |||||
Db    610 AGCCGGGCGTCGGTGATCCAGGCTTTCTTGGGCTCAGCCCCCCAGCTGACCCTACAGCTG 669

Qy    565 TATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTAATGGTATTTTCC 624
          ||  | ||  | ||        || ||  |  | || |||  | | || |||    | |||
Db    670 TACATAAGTGTCATGCAGCAGGACGTCACTGTTGGAAGAAGTCTCCTCATGACCATATCC 729

Qy    625 CTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGATCAAGTAC 684
          ||| | ||  |   ||||| |||   | ||||| ||  | || ||| | |||||||||
Db    730 CTGTTGTCCATTGTGTATGGAGCCTTGCGCTGCAACATCCTAGCCATCAAAATCAAGTAC 789

Qy    685 GATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTGGCGGACA 744
          |||||  ||  |  |     |  ||| ||  |      |||| |||  | | ||| |||
Db    790 GATGAGTATGAAGTCAAAGTGAAGCCTCTGGCCTATGTCTGTATCTTCCTGTGGAGGAGC 849

Qy    745 TTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAAATTGAAG 804
          ||  |||||  |  | ||  |  |  | ||||| |||||  |  ||     ||||      |
Db    850 TTTGAGATTGCCACTCGAGTTGTAGTCCTGGTCCTCTTTACCTCCGTCCTGAAGACCTGG 909

Qy    805 GCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGATTAAGTTC 864
          |  |||     |  || |  |||||||| | |   || ||||  | |||||||     |||
Db    910 GTGGTGGTTATAATACTCATCAACTTCTTCAGTTTCTTCTTGTACCCCTGGATCCTCTTC 969

Qy    865 TGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGTCGGCACT 924
          |||  | ||||||  |||   | ||  | |||||  |||||    | ||||   | ||  |||||
Db    970 TGGTGCAGTGGTTCCCCATTCCCTGAGAACATAGAGAAGGCCCTCAGTAGAGTGGGCACC 1029
```

```
Qy     925 CTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTGCTGGTCA 984
Db    1030 ACCATTGTACTATGCTTTCTAACTTTACTCTATACTGGTATCAACATGTTCTGCTGGTCT 1089

Qy     985 GCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTGGGGACAT 1044
Db    1090 GCTGTACAGCTGAAAATTGACAGCCCTGACCTCATCAGCAAGTCCCATAATTGGTACCAG 1149

Qy    1045 ATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGTTTTTAAG 1104
Db    1150 CTACTGGTGTATTACATGATAAGATTCATCGAGAATGCCATCCTCCTCCTCCTGTGGTAT 1209

Qy    1105 TTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCAGCTCATT 1164
Db    1210 CTTTTCAAGACTGACATCTATATGTATGTGTGCGCACCTCTGTTGGTCCTGCAGCTGCTC 1269

Qy    1165 ATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCATCCATTG 1224
Db    1270 ATTGGGTACTGCACAGCCATTCTCTTCATGCTTGTATTCTATCAGTTCTTCCACCCTTGC 1329

Qy    1225 CGCTCACTCTTCACCCATAATGTAGTAGACTACCTCCA 1262
Db    1330 AAAAAGCTCTTTTCTTCCAGTGTTTCTGAAGGCTTTCA 1367
```

RESULT 5
ABA46582
ID ABA46582 standard; DNA; 668 BP.
XX
AC ABA46582;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human breast cell single exon nucleic acid probe #5277.
XX
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
PS Claim 4; SEQ ID NO 5277; 327pp + sequence listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

```
  Query Match             20.0%;  Score 270.6;  DB 22;  Length 668;
  Best Local Similarity   65.1%;  Pred. No. 1.5e-72;
  Matches  399;  Conservative    0;  Mismatches  214;  Indels    0;  Gaps    0;

Qy     618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
Db       2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy     678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
Db      62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy     738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
Db     122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy     798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
Db     182 ACTGAAGAGCCTACCCGTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy     858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
Db     242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy     918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
Db     302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy     978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
Db     362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy    1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
Db     422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy    1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
Db     482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy    1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
Db     542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy    1218 TCCATTGCGCTCA 1230
Db     602 CCCATGGCAGTCA 614
```

RESULT 6
ABA64445
ID ABA64445 standard; DNA; 668 BP.
XX
AC ABA64445;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #12750.
XX

```
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 4; SEQ ID NO 12750; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

  Query Match           20.0%;  Score 270.6;  DB 22;  Length 668;
  Best Local Similarity  65.1%;  Pred. No. 1.5e-72;
  Matches  399;  Conservative    0;  Mismatches  214;  Indels    0;  Gaps    0;

Qy     618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
           |||||||||| |||| || || ||||||||||  |  ||||||||  |||| |||||||| 
Db       2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy     678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
           ||   | |||||    |  |||   ||   |||  ||||| || ||||  ||   || ||
Db      62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy     738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
           |||    |||||| | |  || ||  |  ||| |||||    | |||   ||  || ||||
Db     122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy     798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
           | |||||    | ||| |  |  |  |||  |   |  |     | || |  || ||| |
Db     182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy     858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
             |||| |||| |||||| || ||  | ||.    ||||  || || || | ||    |||
Db     242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy     918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
           || ||  |  || | ||  | |   ||||  | || ||||||| ||||||||||| ||
Db     302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy     978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
           |||||||||  || |  ||  |||| ||||     |  |  | |||    | ||||  ||
Db     362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy    1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
           ||| ||||    ||| ||||| ||  |   |||  |||| |||||||| ||| | |||||
Db     422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy    1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
           |||| |||||||||||| ||||   || |||||||  ||| | || || |||||| ||||
Db     482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy    1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
           |||||| ||    || ||  |  ||| || ||| |||||||| ||||  ||||| ||| |
Db     542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy    1218 TCCATTGCGCTCA 1230
           |||| ||  |||
Db     602 CCCATGGCAGTCA 614


RESULT 7
ABA31582
ID   ABA31582 standard; DNA; 668 BP.
XX
AC   ABA31582;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #10048 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 4; SEQ ID No 10048; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;
```

Query Match 20.0%; Score 270.6; DB 22; Length 668;
Best Local Similarity 65.1%; Pred. No. 1.5e-72;
Matches 399; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

```
Qy    618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
          ||||||||||| |||| || || ||||||||||  |  ||||||||  |||| ||||||||
Db      2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy    678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
          ||   | |||||     |  |||    ||   |||  ||||| || ||||  ||    || ||
Db     62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy    738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
          |||    |||||| | |  || ||  |  ||| |||||  | |||   ||  || ||||
Db    122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy    798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
          | |||||    | ||| |  |  |  |||  |   |  |     | || |  || ||| |
Db    182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy    858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
          ||||  |||| |||||| || ||  | ||    ||||  || || || | ||    |||
Db    242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy    918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
          || ||  |  || | ||  | |   ||||  | || |||||||  ||||||||||||| ||
Db    302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy    978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
          |||||||||  || |  ||  |||| ||||     |  |  | |||    | ||||  ||
Db    362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy   1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
          |||  ||||    ||| ||||| ||  |   |||  |||| |||||||| ||| | |||||
Db    422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy   1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
          ||||  |||||||||||| ||||   || |||||||  ||| | || || |||||| ||||
Db    482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy   1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
          ||||||  ||    || ||  |  ||| || ||| |||||||| ||||  |||||  ||| |
Db    542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy   1218 TCCATTGCGCTCA 1230
          ||||  ||  |||
Db    602 CCCATGGCAGTCA 614
```

RESULT 8
AAK12903
ID AAK12903 standard; DNA; 668 BP.
XX
AC AAK12903;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 12894.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 12894; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

Query Match 20.0%; Score 270.6; DB 22; Length 668;
Best Local Similarity 65.1%; Pred. No. 1.5e-72;
Matches 399; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

Qy 618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
Db 2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy 678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
Db 62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy 738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
Db 122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy 798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
Db 182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy 858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
Db 242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy 918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
Db 302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy 978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
Db 362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy 1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
Db 422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy 1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
Db 482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy 1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
Db 542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy 1218 TCCATTGCGCTCA 1230
Db 602 CCCATGGCAGTCA 614

```
Db    602 CCCATGGCAGTCA 614


RESULT 9
AAK38630
ID   AAK38630 standard; DNA; 668 BP.
XX
AC   AAK38630;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed single exon probe SEQ ID NO: 13187.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00668.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human bone marrow -
XX
PS   Example 4; SEQ ID NO: 13187; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC   the probes of the invention.
XX
SQ   Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

  Query Match             20.0%;  Score 270.6;  DB 22;  Length 668;
  Best Local Similarity   65.1%;  Pred. No. 1.5e-72;
  Matches  399;  Conservative    0;  Mismatches  214;  Indels    0;  Gaps    0;

Qy    618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
          |||||||||| |||| || || |||||||||| |  ||||||||  |||| ||||||||
Db      2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy    678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
          ||   | |||||    |  |||   ||   |||  ||||| || ||||  ||   || ||
Db     62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy    738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
          |||    ||||||  |  |  || ||  |  ||| |||||   | |||   ||  || ||||
Db    122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy    798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
          | |||||    | ||| |  |  |  |||  |   |  |      | || |  || ||| |
Db    182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy    858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
          |||| |||| |||||| || ||  | ||    ||||  || || || | ||    |||
Db    242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy    918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
          || ||  |  || | ||  | |  ||||  | || |||||| ||||||||||| ||
Db    302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy    978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
          |||||||||  || |  ||  |||| ||||      |  |  | |||     | ||||  ||
Db    362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy   1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
          |||  ||||    ||| ||||| ||  |   |||  |||| |||||||| ||| | |||||
Db    422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy   1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
          ||||  |||||||||||  ||||   || |||||||  |||  | ||  || |||||  ||||
Db    482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy   1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
          ||||||  ||    ||  ||  |  ||| ||  ||| |||||||| ||||  ||||| ||| |
Db    542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy   1218 TCCATTGCGCTCA 1230
          ||||  ||  |||
Db    602 CCCATGGCAGTCA 614


RESULT 10
AAI19430
ID   AAI19430 standard; DNA; 668 BP.
XX
AC   AAI19430;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #9363 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 25; SEQ ID No 9363; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
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CC   expression, the probes are therefore useful in grading and/or staging
CC   of diseases of the cervix, notably cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

  Query Match             20.0%;  Score 270.6;  DB 22;  Length 668;
  Best Local Similarity   65.1%;  Pred. No. 1.5e-72;
  Matches  399;  Conservative    0;  Mismatches  214;  Indels    0;  Gaps    0;

Qy     618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
           |||||||||| |||| || || |||||||||| |  ||||||||  |||| ||||||||
Db       2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy     678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
           ||   | |||||    |  |||   ||   |||  ||||| || ||||  ||   || ||
Db      62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy     738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
           |||    |||||| | |  || ||  |  ||| |||||   | |||   ||  || ||||
Db     122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy     798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
           | |||||   | ||| | |  |  |||  |  |  |     | || |  || ||| |
Db     182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy     858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
             |||| |||| |||||| || ||  | ||    ||||  || || || | ||    |||
Db     242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy     918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
           || ||  |  || | ||  | |   ||||  | || |||||| ||||||||||| ||
Db     302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy     978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
           |||||||||  || |  ||  |||| ||||     |  | | |||    | ||||  ||
Db     362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy    1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
           |||  ||||    ||| ||||| ||  |   ||| |||| |||||||| ||| | |||||
Db     422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy    1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
           |||| ||||||||||| ||||   || |||||||  ||| | || || |||||| ||||
Db     482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy    1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
           |||||| ||    || ||  |  ||| || ||| |||||||| ||||  ||||| ||| |
Db     542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy    1218 TCCATTGCGCTCA 1230
           |||| ||  |||
Db     602 CCCATGGCAGTCA 614


RESULT 11
AAI44621
ID   AAI44621 standard; DNA; 668 BP.
XX
AC   AAI44621;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Probe #13307 used to measure gene expression in human placenta sample.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00663.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta -
XX
PS   Claim 25; SEQ ID No 13307; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENP).
CC   The present sequence is one such probe. The probes are useful for
CC   producing a microarray for predicting, measuring and displaying gene
CC   expression in samples derived from human placenta. The probes are useful
CC   for antenatal diagnosis of human genetic disorders.
XX
SQ   Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

  Query Match             20.0%;  Score 270.6;  DB 22;  Length 668;
  Best Local Similarity   65.1%;  Pred. No. 1.5e-72;
  Matches  399;  Conservative    0;  Mismatches  214;  Indels    0;  Gaps    0;

Qy     618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
           |||||||||| |||| || || |||||||||| |  ||||||||  |||| ||||||||
Db       2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy     678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
           ||   | |||||    |  |||   ||   |||  ||||| || ||||  ||   || ||
Db      62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy     738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
           |||    |||||| | |  || ||  |  ||| |||||   | |||   ||  || ||||
Db     122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy     798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
           | |||||   | ||| | |  |  |||  |  |  |     | || |  || ||| |
Db     182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy     858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
             |||| |||| |||||| || ||  | ||    ||||  || || || | ||    |||
Db     242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy     918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
           || ||  |  || | ||  | |   ||||  | || |||||| ||||||||||| ||
Db     302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy     978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
           |||||||||  || |  ||  |||| ||||     |  | | |||    | ||||  ||
Db     362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy    1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
           |||  ||||    ||| ||||| ||  |   ||| |||| |||||||| ||| | |||||
Db     422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy    1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
           |||| ||||||||||| ||||   || |||||||  ||| | || || |||||| ||||
Db     482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy    1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
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```
Db    542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy   1218 TCCATTGCGCTCA 1230
Db    602 CCCATGGCAGTCA 614
```

RESULT 12
AAI05155
ID AAI05155 standard; DNA; 668 BP.
XX
AC AAI05155;
XX
DT 09-OCT-2001 (first entry)
XX
DE Probe #5146 used to measure gene expression in human breast sample.
XX
KW Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US00661.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
PS Claim 25; SEQ ID No 5146; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

Query Match 20.0%; Score 270.6; DB 22; Length 668;
Best Local Similarity 65.1%; Pred. No. 1.5e-72;
Matches 399; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

```
Qy    618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
Db      2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy    678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
Db     62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy    738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
Db    122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy    798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
Db    182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy    858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
Db    242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy    918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
Db    302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy    978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
Db    362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy   1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
Db    422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy   1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
Db    482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy   1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
Db    542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy   1218 TCCATTGCGCTCA 1230
Db    602 CCCATGGCAGTCA 614
```

RESULT 13
ABS12699
ID ABS12699 standard; DNA; 668 BP.
XX
AC ABS12699;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 12690.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesis; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.

PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
PS Claim 4; SEQ ID No 12690; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe open reading frame of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 668 BP; 171 A; 136 C; 146 G; 215 T; 0 other;

Query Match 20.0%; Score 270.6; DB 24; Length 668;
Best Local Similarity 65.1%; Pred. No. 1.5e-72;
Matches 399; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

```
Qy    618 ATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATCCAGAT 677
          ||||||||||| |||| || || |||||||||||  |  ||||||||  |||| |||||||||
Db      2 ATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAATATACTGGCCATCCAGAT 61

Qy    678 CAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTG 737
          ||   | |||||    | |||   ||   |||  ||||| || ||||  ||   || ||
Db     62 CAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTCTTCTGTGTCGTGATGTG 121

Qy    738 GCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAA 797
          |||    |||||| | |  || ||  |  ||| |||||   | |||  ||  || ||||
Db    122 GCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTTTTCATTGCATCTCTGAA 181

Qy    798 ATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAGCCCTGGAT 857
          | |||||    | ||| |  |  | |||  |   |  |     | ||  |  || ||| |
Db    182 ACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCATTGTTGGCACCGTGGCT 241

Qy    858 TAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGT 917
            |||| |||| |||||| || ||  | ||    ||||  || || || | ||    |||
Db    242 GGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAAAATAATTCCAATATGGT 301

Qy    918 CGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTG 977
          || ||  |  || | ||  | |   |||| | || |||||||·||||||||||||| ||
Db    302 GGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCTGCCATCAACTTCTCCTG 361

Qy    978 CTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTG 1037
          |||||||||  || |  ||  |||| ||||      | |  | |||     | ||||  ||
Db    362 CTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATTGACGGGAGACAGAGGTG 421

Qy   1038 GGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGT 1097
          |||  ||||    ||| ||||| ||  |   |||  |||| |||||||| ||| | |||||
Db    422 GGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTAGAAAATGTGATAATGATATTGGT 481

Qy   1098 TTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCA 1157
            |||| |||||||||| ||||   || |||||||  ||| | || || |||||| ||||
Db    482 ATTTAGGTTCTTTGGAGGGAAAACTTTGCTGAATTGTTGTGACTCATTAATTGCCGTGCA 541

Qy   1158 GCTCATTATTGCTTATCTGATTTCCATTGACTTCATGCTCCTTTTCTTCCAGTACTTGCA 1217
          |||||| ||    || ||  |  ||| || ||| |||||||| ||||  ||||| ||| |
Db    542 GCTCATCATAAGCTACCTATTGGCCACTGGCTTTATGCTCCTCTTCTATCAGTATTTGTA 601

Qy   1218 TCCATTGCGCTCA 1230
          |||| ||  |||
Db    602 CCCATGGCAGTCA 614
```

RESULT 14
ABA51767
ID ABA51767 standard; DNA; 471 BP.
XX
AC ABA51767;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #72.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
PS Claim 1; SEQ ID NO 72; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for

CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 471 BP; 117 A; 94 C; 104 G; 156 T; 0 other;

Query Match 13.1%; Score 176.8; DB 22; Length 471;
Best Local Similarity 61.9%; Pred. No. 9.4e-44;
Matches 280; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 601 AGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAAT 660
Db 19 ATAGCATTGCTGATGACATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAAT 78

Qy 661 ATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTC 720
Db 79 ATACTGGCCATCCAGATCAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTC 138

Qy 721 CTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTC 780
Db 139 TTCTGTGTCGTGATGTGGCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTT 198

Qy 781 TTCTCAGCCACTTTGAAATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATC 840
Db 199 TTCATTGCATCTCTGAAACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCA 258

Qy 841 CTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAG 900
Db 259 TTGTTGGCACCGTGGCTGGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAA 318

Qy 901 AAAAACTTCAGCCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCT 960
Db 319 AATAATTCCAATATGGTGGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCT 378

Qy 961 GGCATCAACTTCTCTTGCTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTC 1020
Db 379 GCCATCAACTTCTCCTGCTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATT 438

Qy 1021 GACAAAGGGCAGAACTGGGGACATATGGGCCT 1052
Db 439 GACGGGAGACAGAGGTGGGGCCATAGAATCCT 470

RESULT 15
ABA21596
ID ABA21596 standard; DNA; 471 BP.
XX
AC ABA21596;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #62 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 1; SEQ ID No 62; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 471 BP; 117 A; 94 C; 104 G; 156 T; 0 other;

Query Match 13.1%; Score 176.8; DB 22; Length 471;
Best Local Similarity 61.9%; Pred. No. 9.4e-44;
Matches 280; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 601 AGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAAT 660
Db 19 ATAGCATTGCTGATGACATTTTCCCTGTTATCAGTTACTTATGGGGCCATTCGCTGCAAT 78

Qy 661 ATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTC 720
Db 79 ATACTGGCCATCCAGATCAGCAATGATGATACTACCATTAAGCTACCGCCGATAGAATTC 138

Qy 721 CTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTC 780
Db 139 TTCTGTGTCGTGATGTGGCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTT 198

Qy 781 TTCTCAGCCACTTTGAAATTGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATC 840
Db 199 TTCATTGCATCTCTGAAACTGAAGAGCCTACCCGTTTTGTTAATCATATATTTTGTATCA 258

Qy 841 CTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAG 900
Db 259 TTGTTGGCACCGTGGCTGGAGTTTTGGAAAAGTGGAGCTCATCTTCCTGGCAACAAAGAA 318

Qy 901 AAAAACTTCAGCCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCT 960
Db 319 AATAATTCCAATATGGTGGGTACAGTACTGATGCTTTTCTTGATCACACTGCTATATGCT 378

Qy 961 GGCATCAACTTCTCTTGCTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTC 1020
Db 379 GCCATCAACTTCTCCTGCTGGTCAGCAGTGAAACTGCAGTTGTCAGATGACAAAATAATT 438

Qy 1021 GACAAAGGGCAGAACTGGGGACATATGGGCCT 1052
Db 439 GACGGGAGACAGAGGTGGGGCCATAGAATCCT 470

Search completed: March 30, 2003, 03:16:38
Job time : 245.597 secs